



Attachment
9/c

SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
THEREFOR

<130> HAR-005

<140> 09/248,964

<141> 1999-02-12

<150> PCT/US97/14503

<151> 1997-08-15

<150> 60/075,351

<151> 1998-02-19

<150> 60/024,007

<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> CDS

<222> (1)..(735)

<220>

<221> misc_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc_structure

<222> (22)..(594)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (595)..(615)

<223> Linker sequence

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<221> misc_feature

<222> (616)..(735)





<223> Fos leucine zipper domain

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gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac	96
Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp	
20 25 30	
ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg	144
Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr	
35 40 45	
gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa	192
Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln	
50 55 60	
ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg	240
Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met	
65 70 75 80	
aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta	288
Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val	
85 90 95	
act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc	336
Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu	
100 105 110	
atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg	384
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp	
115 120 125	
ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc	432
Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe	
130 135 140	
ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc	480
Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe	
145 150 155 160	
ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc	528
Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly	
165 170 175	
ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct	576
Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro	
180 185 190	
ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat	624
Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp	
195 200 205	
aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg	672
Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu	

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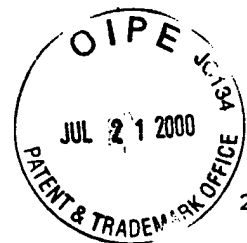
JUL 31 2000

TECH CENTER 1600/2900

RECEIVED

JUL 28 2000

TECH CENTER 1600/2900



210

215

220

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac 750
Ile Leu Ala Ala His
245

<210> 2

<211> 245

<212> PRT

<213> Artificial Sequence

<400> 2

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
1 5 10 15

Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
50 55 60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
65 70 75 80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
85 90 95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
100 105 110

Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
115 120 125

Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
130 135 140

Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145 150 155 160

Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
165 170 175

Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
180 185 190

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
195 200 205

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu



210

215

220

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

Ile Leu Ala Ala His
245

<210> 3

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR@-Jun fusion

<220>

<221> CDS

<222> (1)..(756)

<220>

<221> misc_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc_feature

<222> (22)..(615)

<223> DRB1*1501 extracellular domain

<220>

<221> misc_feature

<222> (616)..(636)

<223> Linker sequence

<220>

<221> misc_feature

<222> (637)..(756)

<223> Jun leucine zipper domain

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1 5 10 15

cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg 96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac 144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
35 40 45

agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac 192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60



gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc 240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
65 70 75 80

gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc 288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag 336
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt 384
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa 432
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg 480
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag 528
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca 576
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga 624
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

ggg ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg 672
Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa 720
Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac 771
Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
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<210> 4

<211> 252

<212> PRT

<213> Artificial Sequence

<400> 4

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5

10

15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

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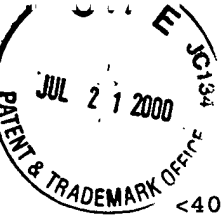
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic PCR
primer



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42

<210> 6

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic PCR primer

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gtcatagaat tctcaatggg cggccaggat gaactccag

39

<210> 7

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

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gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc

42

<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 8

gtcatagaat tctcaatggt tcatgacttt ctgtttaag

39

<210> 9

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic, biotin ligase recognition sequence

<400> 9

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp

1

5

10



<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
linker sequence

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Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
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<210> 11
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (1)..(15)
<223> 3' end of secretory signal

<220>
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<222> (16)..(588)
<223> DRA*0101 extracellular domain

<220>
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<222> (589)..(609)
<223> Linker

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<223> Fos leucine zipper domain

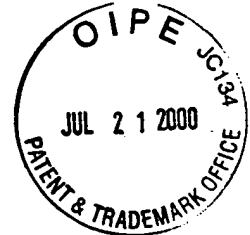
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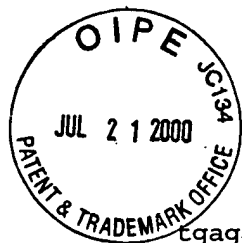
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ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg	144															
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp																
35 40 45																
cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca	192															
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala																
50 55 60																
ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag	240															
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys																
65 70 75 80																
cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg	288															
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val																
85 90 95																
ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt	336															
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys																
100 105 110																
ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga	384															
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg																
115 120 125																
aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc	432															
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro																
130 135 140																
agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc	480															
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro																
145 150 155 160																
tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat	528															
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp																
165 170 175																
gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca	576															
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro																
180 185 190																
gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc	624															
Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu																
195 200 205																
caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc	672															
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr																
210 215 220																
gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg	720															
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu																
225 230 235 240																
gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt	768															
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys																



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cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc				816
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val				
260	265	270		
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc				864
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser				
275	280	285		
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat				912
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp				
290	295	300		
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag				960
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln				
305	310	315	320	
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt				1008
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser				
325	330	335		
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa				1056
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys				
340	345	350		
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc				1104
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile				
355	360	365		
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct				1152
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro				
370	375	380		
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg				1200
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met				
385	390	395	400	
gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac				1248
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn				
405	410	415		
ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct				1296
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser				
420	425	430		
gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac				1344
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn				
435	440	445		
tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg				1392
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu				
450	455	460		
cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa				1437
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys				
465	470	475		



tgagaattc

1446

<210> 12
<211> 479
<212> PRT
<213> Artificial Sequence

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20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu
195 200 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
210 215 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
245 250 255



Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
275 280 285

Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
290 295 300

Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305 310 315 320

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
325 330 335

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
340 345 350

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
355 360 365

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
370 375 380

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385 390 395 400

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
405 410 415

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
435 440 445

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
450 455 460

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465 470 475

<210> 13

<211> 1851

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> CDS

<222> (1) .. (1836)

<220>



<221> misc_feature
<222> (1)..(75)
<223> 3' end of secretory signal

<220>
<221> misc_feature
<222> (76)..(648)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (649)..(669)
<223> Linker

<220>
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<222> (670)..(789)
<223> Fos leucine zipper domain

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<223> IgG domain

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Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
20 25 30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
35 40 45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag 240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa 288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca 336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac 384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125



ctc	atc	tgt	ttc	ata	gac	aag	ttc	acc	cca	cca	gtg	gtc	aat	gtc	432	
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	
130						135					140					
acg	tgg	ctt	cga	aat	gga	aaa	cct	gtc	acc	aca	gga	gtg	tca	gag	aca	480
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145					150					155					160	
gtc	ttc	ctg	ccc	agg	gaa	gac	cac	ctt	ttc	cgc	aag	ttc	cac	tat	ctc	528
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	
				165					170					175		
ccc	ttc	ctg	ccc	tca	act	gag	gac	gtt	tac	gac	tgc	agg	gtg	gag	cac	576
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	
			180					185					190			
tgg	ggc	ttg	gat	gag	cct	ctt	ctc	aag	cac	tgg	gag	ttt	gat	gct	cca	624
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	
		195					200					205				
agc	cct	ctc	cca	gag	act	aca	gag	gtc	gac	gga	ggg	ggc	ggc	ggg	tta	672
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu	
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act	gat	aca	ctc	caa	gcg	gag	aca	gat	caa	ctt	gaa	gac	gag	aag	tct	720
Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser	
	225				230				235						240	
gcg	ttg	cag	acc	gag	att	gcc	aat	cta	ctg	aaa	gag	aag	gaa	aaa	ctg	768
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu	
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Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn	
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gtg	ttc	gtc	cca	cca	cgg	gat	ggc	ttc	tct	ggc	cct	gca	cca	cgc	aag	864
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys	
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tct	aaa	ctc	atc	tgc	gag	gcc	acg	aac	ttc	act	cca	aaa	ccg	atc	aca	912
Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr	
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gta	tcc	tgg	cta	aag	gat	ggg	aag	ctc	gtg	gaa	tct	ggc	ttc	acc	aca	960
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr	
	305				310					315					320	
gat	ccg	gtg	acc	atc	gag	aac	aaa	gga	tcc	aca	ccc	caa	acc	tac	aag	1008
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys	
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gtc	ata	agc	aca	ctt	acc	atc	tct	gaa	atc	gac	tgg	ctg	aac	ctg	aat	1056
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn	
			340					345					350			
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Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn	
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gtg	tcc	tcc	aca	tgt	gct	gcc	agt	ccc	tcc	aca	gat	atc	ctt	aat	ttt	1152
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe	
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act	att	cct	cct	tcc	ttt	gcc	gac	atc	ttc	ctt	agc	aag	tcc	gct	aac	1200
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn	
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Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile	
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tcc	tgg	gct	tct	caa	agt	ggc	gaa	cca	ctg	gaa	acc	aaa	att	aaa	atc	1296
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile	
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atg	gaa	agc	cat	ccc	aat	ggc	acc	ttc	agt	gct	aag	ggc	gtg	gct	agt	1344
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser	
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Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val	
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Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro	
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Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala	
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cgt	gaa	caa	ctg	aac	ctg	agg	gag	tca	gcc	aca	gtc	acc	tgc	ctg	gtg	1536
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val	
			500					505					510			
aag	ggc	ttc	tct	cct	gca	gac	atc	tct	gtg	caa	tgg	aag	cag	agg	ggc	1584
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly	
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cag	ctc	tta	ccc	cag	gag	aag	tat	gtg	acc	agt	gcc	ccg	atg	cca	gag	1632
Gln	Leu	Leu	Pro	Gln	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	
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Pro	Gly	Ala	Pro	Gly	Phe	Tyr	Phe	Thr	His	Ser	Ile	Leu	Thr	Val	Thr	
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Glu	Glu	Glu	Trp	Asn	Ser	Gly	Glu	Thr	Tyr	Thr	Cys	Val	Val	Gly	His	
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gag	gcc	ctg	cca	cac	ctg	gtg	acc	gag	agg	acc	gtg	gac	aag	tcc	act	1776
Glu	Ala	Leu	Pro	His	Leu	Val	Thr	Glu	Arg	Thr	Val	Asp	Lys	Ser	Thr	



580 585 590
ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc 1824
Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

ggc acc tgc tat tgaagatctg tcgac 1851
Gly Thr Cys Tyr
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Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
35 40 45
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu



210					215					220					
Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser
225					230					235					240
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu
				245					250					255	
Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn
			260					265					270		
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys
		275					280					285			
Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr
	290						295				300				
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr
305					310					315					320
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys
				325					330					335	
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn
			340					345					350		
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn
		355					360					365			
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe
	370					375					380				
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn
385					390					395					400
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile
			405						410					415	
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Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val
	450					455					460				
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro
465					470					475					480
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala
			485						490					495	
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val
			500					505					510		
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly



515

520

525

Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
530 535 540

Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545 550 555 560

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

C1
included Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610
